

SEQUENCE LISTING

<110> TAKEDA, Junji
 HORIE, Kyoji
 YUSA, Kosuke
 ISHIHARA, Hiroshi

<120> DEVELOPMENT OF MAMMALIAN GENOME MODIFICATION TECHNIQUE
 USING RETROTRANSPONSON

<130> 710048.401USPC

<140> US 10/579,936
 <141> 2004-11-19

<150> PCT/JP2004/017307
 <151> 2004-11-19

<150> JP 2003-393175
 <151> 2003-11-21

<160> 47

<170> PatentIn version 3.2

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1640

1645

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ttctttgatt	ggtctgtaag	cttaaggccc	aaactaagag	agacaagggtg	gttattgccc	6454
aggcgcttgc	aggactagaa	catggagctt	cccctgatat	atctatgctt	aagcaatagg	6514
tcgctggcca	ctcagctctt	atatctcacg	aggctagtct	cattgcacga	gatagagtga	6574
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ctctctcttg	cttccctctc	ttgcttcttg	ctctctcttg	cttccctctc	ttgcttcttg	7174
ctctctcttg	cttccctctc	ttgcttcttg	ctctctcttg	cttcttgctc	tcttttccctg	7234
aagatgtaag	aataaagctt	tgtcgcagaa	gattctggct	tgtgggtgttc	ttcctggccg	7294
gtcgtgagaa	cgcgtcgaat	aaca				7318

<210> 2

<211> 586

<212> PRT

<213> Mus musculus

<220>

<223> IAP sequence amino acid sequence (gag #1)

<400> 2

Met	Asn	Ser	Glu	Leu	Phe	Ser	Trp	Gly	Thr	Arg	Val	Pro	Val	Ser	Met
1			5					10					15		
Phe	Gly	Leu	Glu	Phe	Phe	Leu	Val	Leu	Gly	Ala	Leu	Leu	Phe	Leu	Phe
		20						25					30		
Thr	Cys	Tyr	Ile	Val	Val	Lys	Ala	Gly	Leu	Lys	Ile	Leu	Asp	Glu	Ile
		35					40					45			
Gln	Gly	Ser	Leu	Ser	Glu	Val	Lys	Arg	Gly	Glu	Arg	Val	Gly	Ala	Arg
	50					55				60					
Arg	Asn	Gly	Lys	Tyr	Thr	Gly	Leu	Ser	Lys	Gly	Leu	Glu	Pro	Glu	Glu
65					70					75				80	
Lys	Leu	Arg	Leu	Gly	Arg	Asn	Thr	Trp	Arg	Glu	Ile	Arg	Arg	Lys	Arg
			85						90					95	
Gly	Lys	Arg	Glu	Lys	Lys	Lys	Asp	Arg	Leu	Ala	Glu	Val	Ser	Arg	Arg
			100					105						110	

Tyr Ser Ser Leu Asp Glu Leu Arg Lys Pro Ala Leu Ser Ser Ser Glu
 115 120 125
 Ala Ser Glu Glu Ser Ser Ser Glu Glu Thr Asp Trp Glu Glu Glu Ala
 130 135 140

 Ala His Tyr Gln Pro Ala Asn Trp Ser Arg Lys Lys Pro Lys Ala Ala
 145 150 155 160

 Gly Glu Ser Gln Arg Thr Val Gln Pro Pro Gly Ser Arg Phe Gln Gly
 165 170 175

 Pro Pro Tyr Ala Glu Pro Pro Pro Cys Val Val Arg Gln Gln Cys Ala
 180 185 190

 Glu Arg Gln Cys Ala Glu Arg Cys Ala Glu Arg Gln Cys Ala Asp Arg
 195 200 205

 Cys Ala Glu Arg Gln Cys Ala Glu Arg Gln Cys Ala Asp Ser Phe Ile
 210 215 220

 Pro Arg Glu Glu Gln Lys Lys Ile Glu Gln Ala Phe Pro Val Phe Glu
 225 230 235 240

 Gly Ala Glu Gly Gly Arg Val His Ala Pro Val Glu Tyr Val Gln Ile
 245 250 255

 Lys Glu Ile Ala Glu Ser Val Arg Lys Tyr Gly Thr Asn Ala Asn Phe
 260 265 270

 Thr Leu Val Gln Leu Asp Arg Leu Ala Gly Met Ala Leu Thr Pro Ala
 275 280 285

 Asp Trp Gln Thr Val Val Lys Ala Ala Leu Pro Ser Met Gly Lys Tyr
 290 295 300

 Met Glu Trp Lys Ala Leu Trp His Glu Ala Ala Gln Ala Gln Ala Arg
 305 310 315 320

 Ala Asn Ala Ala Ala Leu Thr Pro Glu Gln Arg Asp Trp Thr Phe Asp
 325 330 335

 Leu Leu Thr Gly Gln Gly Ala Tyr Ser Ala Asp Gln Thr Asn Tyr His
 340 345 350

 Trp Gly Ala Tyr Ala Gln Ile Ser Ser Thr Ala Ile Arg Ala Trp Lys
 355 360 365

 Ala Leu Ser Arg Ala Gly Glu Thr Thr Gly Gln Leu Thr Lys Ile Ile
 370 375 380

 Gln Gly Pro Gln Glu Ser Phe Ser Asp Phe Val Ala Arg Met Thr Glu
 385 390 395 400

 Ala Ala Glu Arg Ile Phe Gly Glu Ser Glu Gln Ala Ala Pro Leu Ile

	405		410		415
Glu Gln Leu Ile Tyr Glu Gln Ala Thr Lys Glu Cys Arg Ala Ala Ile	420		425		430
Ala Pro Arg Lys Asn Lys Gly Leu Gln Asp Trp Leu Arg Val Cys Arg	435		440		445
Glu Leu Gly Gly Pro Leu Ser Asn Ala Gly Leu Ala Ala Ala Ile Leu	450		455		460
Gln Ser Gln Asn Arg Ser Met Gly Arg Asn Asp Gln Arg Thr Cys Phe	465		470		475
Asn Cys Gly Lys Pro Gly His Phe Lys Lys Asp Cys Arg Ala Pro Asp	485		490		495
Lys Gln Gly Gly Thr Leu Thr Leu Cys Ser Lys Cys Gly Lys Gly Tyr	500		505		510
His Arg Ala Asp Gln Cys Arg Ser Val Arg Asp Ile Lys Gly Arg Ile	515		520		525
Leu Pro Pro Pro Asp Ser Gln Ser Ala Asp Val Pro Lys Asn Gly Ser	530		535		540
Pro Gly Pro Arg Ser Gln Gly Pro Gln Arg Tyr Gly Asn Arg Phe Val	545		550		555
Arg Thr Gln Glu Ala Val Arg Glu Thr Thr Gln Glu Asp Pro Gln Gly	565		570		575
Trp Thr Cys Val Pro Pro Pro Thr Ser Tyr	580		585		

<210> 3
 <211> 258
 <212> PRT
 <213> Mus musculus

<220>
 <223> IAP sequence amino acid sequence (gag #2)

<400> 3

Met Pro Gln Met Ser Ile Gln Pro Val Pro Val Glu Pro Ile Pro Ser			
1	5	10	15
Leu Pro Pro Gly Thr Met Gly Leu Ile Leu Gly Arg Gly Ser Leu Thr			
20	25	30	
Leu Gln Gly Leu Val Val His Pro Gly Ile Met Asp Cys Gln His Ser			
35	40	45	

Pro Glu Ile Gln Val Leu Cys Ser Ser Pro Lys Gly Val Phe Ser Ile
 50 55 60
 Ser Lys Gly Asp Arg Ile Ala Gln Leu Leu Leu Leu Pro Asp Asn Thr
 65 70 75 80
 Arg Glu Lys Ser Ala Gly Pro Glu Ile Lys Lys Met Gly Ser Ser Gly
 85 90 95
 Asn Asp Ser Ala Tyr Leu Val Val Ser Leu Asn Asp Arg Pro Lys Leu
 100 105 110
 Arg Leu Lys Ile Asn Gly Lys Glu Phe Glu Gly Ile Leu Asp Thr Gly
 115 120 125
 Ala Asp Lys Ser Ile Ile Ser Thr His Trp Trp Pro Lys Ala Trp Pro
 130 135 140
 Thr Thr Glu Ser Ser His Ser Leu Gln Gly Leu Gly Tyr Gln Ser Cys
 145 150 155 160
 Pro Thr Ile Ser Ser Val Ala Leu Thr Trp Glu Ser Ser Glu Gly Gln
 165 170 175
 Gln Gly Lys Phe Ile Pro Tyr Val Leu Pro Leu Pro Val Asn Leu Trp
 180 185 190
 Gly Arg Asp Ile Met Gln His Leu Gly Leu Ile Leu Ser Asn Glu Asn
 195 200 205
 Ala Pro Ser Gly Gly Tyr Ser Ala Lys Ala Lys Asn Ile Met Ala Lys
 210 215 220
 Met Gly Tyr Lys Glu Gly Lys Gly Leu Gly His Gln Glu Gln Gly Arg
 225 230 235 240
 Ile Glu Pro Ile Ser Pro Asn Gly Asn Gln Asp Arg Gln Gly Leu Gly
 245 250 255
 Phe Pro

<210> 4
 <211> 805
 <212> PRT
 <213> Mus musculus
 <220>
 <223> IAP sequence amino acid sequence (pol)
 <400> 4

Met	Asn	Leu	Phe	Gly	Pro	Val	Gln	Arg	Gly	Leu	Pro	Val	Leu	Ser	Ala	
1				5					10					15		
Leu	Pro	Arg	Gly	Trp	Asn	Leu	Ile	Ile	Ile	Asp	Ile	Lys	Asp	Cys	Phe	
			20					25					30			
Phe	Ser	Ile	Pro	Leu	Cys	Pro	Arg	Asp	Arg	Pro	Arg	Phe	Ala	Phe	Thr	
		35					40					45				
Ile	Pro	Ser	Ile	Asn	His	Met	Glu	Pro	Asp	Lys	Arg	Tyr	Gln	Trp	Lys	
	50					55					60					
Val	Leu	Pro	Gln	Gly	Met	Ser	Asn	Ser	Pro	Thr	Met	Cys	Gln	Leu	Tyr	
65					70					75					80	
Val	Gln	Glu	Ala	Leu	Leu	Pro	Val	Arg	Glu	Gln	Phe	Pro	Ser	Leu	Ile	
				85					90					95		
Leu	Leu	Leu	Tyr	Met	Asp	Asp	Ile	Leu	Leu	Cys	His	Lys	Asp	Leu	Thr	
			100					105					110			
Met	Leu	Gln	Lys	Ala	Tyr	Pro	Phe	Leu	Leu	Lys	Thr	Leu	Ser	Gln	Trp	
		115					120					125				
Gly	Leu	Gln	Ile	Ala	Thr	Glu	Lys	Val	Gln	Ile	Ser	Asp	Thr	Gly	Gln	
	130					135					140					
Phe	Leu	Gly	Ser	Val	Val	Ser	Pro	Asp	Lys	Ile	Val	Pro	Gln	Lys	Val	
145					150					155					160	
Glu	Ile	Arg	Arg	Asp	His	Leu	His	Thr	Leu	Asn	Asp	Phe	Gln	Lys	Leu	
				165					170					175		
Leu	Gly	Asp	Ile	Asn	Trp	Leu	Arg	Pro	Phe	Leu	Lys	Ile	Pro	Ser	Ala	
			180					185					190			
Glu	Leu	Arg	Pro	Leu	Phe	Ser	Ile	Leu	Glu	Gly	Asp	Pro	His	Ile	Ser	
		195					200					205				
Ser	Pro	Arg	Thr	Leu	Thr	Leu	Ala	Ala	Asn	Gln	Ala	Leu	Gln	Lys	Val	
	210					215					220					
Glu	Lys	Ala	Leu	Gln	Asn	Ala	Gln	Leu	Gln	Arg	Ile	Glu	Asp	Ser	Gln	
225					230					235					240	
Pro	Phe	Ser	Leu	Cys	Val	Phe	Lys	Thr	Ala	Gln	Leu	Pro	Thr	Ala	Val	
			245						250					255		
Leu	Trp	Gln	Asn	Gly	Pro	Leu	Leu	Trp	Ile	His	Pro	Asn	Val	Ser	Pro	
			260					265					270			
Ala	Lys	Ile	Ile	Asp	Trp	Tyr	Pro	Asp	Ala	Ile	Ala	Gln	Leu	Ala	Leu	

275		280		285
Lys Gly Leu Lys Ala Ala Ile Thr His Phe Gly Gln Ser Pro Tyr Leu				
290		295		300
Leu Ile Val Pro Tyr Thr Ala Ala Gln Val Gln Thr Leu Ala Ala Ala				
305		310		315 320
Ser Asn Asp Trp Ala Val Leu Val Thr Ser Phe Ser Gly Lys Ile Asp				
	325		330	335
Asn His Tyr Pro Lys His Pro Ile Leu Gln Phe Ala Gln Asn Gln Ser				
	340		345	350
Val Val Phe Pro Gln Ile Thr Val Arg Asn Pro Leu Lys Asn Gly Ile				
	355		360	365
Val Val Tyr Thr Asp Gly Ser Lys Thr Gly Ile Gly Ala Tyr Val Ala				
	370		375	380
Asn Gly Lys Val Val Ser Lys Gln Tyr Asn Glu Asn Ser Pro Gln Val				
385		390		395 400
Val Glu Cys Leu Val Val Leu Glu Val Leu Lys Thr Phe Leu Lys Pro				
	405		410	415
Leu Asn Ile Val Ser Asp Ser Cys Tyr Val Val Asn Ala Val Asn Leu				
	420		425	430
Leu Glu Val Ala Gly Val Ile Lys Pro Ser Ser Arg Val Ala Asn Ile				
	435		440	445
Phe Gln Gln Ile Gln Leu Val Leu Leu Ser Arg Arg Ser Pro Val Tyr				
	450		455	460
Ile Thr His Val Arg Ala His Ser Gly Leu Pro Gly Pro Met Ala Leu				
465		470		475 480
Gly Asn Asp Leu Ala Asp Lys Ala Thr Lys Val Val Ala Ala Ala Leu				
	485		490	495
Ser Ser Pro Val Glu Ala Ala Arg Asn Phe His Asn Asn Phe His Val				
	500		505	510
Thr Ala Glu Thr Leu Arg Ser Arg Phe Ser Leu Thr Arg Lys Glu Ala				
	515		520	525
Arg Asp Ile Val Thr Gln Cys Gln Ser Cys Cys Glu Phe Leu Pro Val				
	530		535	540
Pro His Val Gly Ile Asn Pro Arg Gly Ile Arg Pro Leu Gln Val Trp				
545		550		555 560
Gln Met Asp Val Thr His Val Ser Ser Phe Gly Lys Leu Gln Tyr Leu				

565					570					575					
His	Val	Ser	Ile	Asp	Thr	Cys	Ser	Gly	Ile	Met	Phe	Ala	Ser	Pro	Leu
			580					585					590		
Thr	Gly	Glu	Lys	Ala	Ser	His	Val	Ile	Gln	His	Cys	Leu	Glu	Ala	Trp
		595					600					605			
Ser	Ala	Trp	Gly	Lys	Pro	Arg	Leu	Leu	Lys	Thr	Asp	Asn	Gly	Pro	Ala
	610					615					620				
Tyr	Thr	Ser	Gln	Lys	Phe	Gln	Gln	Phe	Cys	Arg	Gln	Met	Asp	Val	Thr
625					630					635					640
His	Leu	Thr	Gly	Leu	Pro	Tyr	Asn	Pro	Gln	Gly	Gln	Gly	Ile	Val	Glu
			645						650					655	
Arg	Ala	His	Arg	Thr	Leu	Lys	Ala	Tyr	Leu	Ile	Lys	Gln	Lys	Arg	Gly
			660					665					670		
Thr	Phe	Glu	Glu	Thr	Val	Pro	Arg	Ala	Pro	Arg	Val	Ser	Val	Ser	Leu
		675					680					685			
Ala	Leu	Phe	Thr	Leu	Asn	Phe	Leu	Asn	Ile	Asp	Ala	His	Gly	His	Thr
	690					695					700				
Ala	Ala	Glu	Arg	His	Cys	Ser	Glu	Pro	Asp	Arg	Pro	Asn	Glu	Met	Val
705					710					715					720
Lys	Trp	Lys	Asn	Val	Leu	Asp	Asn	Lys	Trp	Tyr	Gly	Pro	Asp	Pro	Ile
			725						730					735	
Leu	Ile	Arg	Ser	Arg	Gly	Ala	Ile	Cys	Val	Phe	Pro	Gln	Asn	Glu	Asp
			740					745					750		
Asn	Pro	Phe	Trp	Val	Pro	Glu	Arg	Leu	Thr	Arg	Lys	Ile	Gln	Thr	Asp
		755					760					765			
Gln	Gly	Asn	Thr	Asn	Val	Pro	Arg	Leu	Gly	Asp	Val	Gln	Gly	Val	Asn
	770					775					780				
Asn	Lys	Glu	Arg	Ala	Ala	Leu	Gly	Asp	Asn	Val	Asp	Ile	Ser	Thr	Pro
785					790					795					800
Asn	Asp	Gly	Asp	Val											
			805												

<210> 5
 <211> 673
 <212> DNA
 <213> Mus musculus
 <220>

<223> CMV promoter sequence

```
<400> 5
tggccattgc atacgttgta tccatatcat aatatgtaca tttatattgg ctcatgtcca    60
acattaccgc catgttgaca ttgattattg actagttatt aatagtaatc aattacgggg    120
tcattagttc atagcccata tatggagttc cgcattacat aacttacggg aaatggcccg    180
cctggctgac cgcccaacga ccccgccca ttgacgtcaa taatgacgta tgttcccata    240
gtaacgcaa tagggacttt ccattgacgt caatgggtgg agtattttac gtaaactgcc    300
cacttggcag tacatcaagt gtatcatatg ccaagtacgc cccctattga cgtcaatgac    360
ggtaaatggc cgcctggga ttatgccag tacatgacct tatgggactt tcctacttgg    420
cagtacatct acgtattagt catcgctatt accatggtga tgcggttttg gcagtacatc    480
aatgggcgtg gatagcgggt tgactcacgg ggatttccaa gtctccacc cattgacgtc    540
aatgggagtt tgttttggca ccaaaatcaa cgggactttc caaaatgtcg taacaactcc    600
gccccattga cgcaaatggg cggtaggcgt gtacgggtgg aggtctatat aagcagagct    660
cgtttagtga acc                                         673
```

<210> 6

<211> 655

<212> DNA

<213> Mus musculus

<220>

<223> CA1 promoter sequence (without the R region and with two bases deletion in the promoter region in addition thereto)

```
<400> 6
attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat    60
atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgccaacg    120
acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt    180
tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag    240
tgtatcatat gccaaagtac cccctattg acgtcaatga cggtaaatgg cccgcctggc    300
attatgccca gtacatgacc ttatgggact ttctacttgg gcagtacatc tacgtattag    360
tcacgctat taccatgggt cgaggtgagc cccacgttct gcttactct ccccatctcc    420
ccccctccc caccccaat tttgtattta tttatttttt aattattttg tgcagcgatg    480
ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg    540
ggcagggcgg agaggtgcgg cggcagccaa tcagagcggc gcgtccgaa agtttctttt    600
tatggcgagg cggcgggcgg gcgcggccca taaaagcga agcgcgcggc gggcg      655
```

<210> 7

<211> 657

<212> DNA

<213> Mus musculus

<220>

<223> CA2 promoter sequence (without the R region)

```
<400> 7
attgattatt gactagttat taatagtaat caattacggg gtcattagtt catagcccat    60
atatggagtt ccgcgttaca taacttacgg taaatggccc gcctggctga ccgccaacg    120
acccccgccc attgacgtca ataatgacgt atgttcccat agtaacgcca atagggactt    180
tccattgacg tcaatgggtg gactatttac ggtaaactgc ccacttggca gtacatcaag    240
tgtatcatat gccaaagtac cccctattg acgtcaatga cggtaaatgg cccgcctggc    300
```

```

attatgccca gtacatgacc ttatgggact ttcctacttg gcagtacatc tacgtattag 360
tcatcgctat taccatgggt cgaggtgagc cccacgttct gcttcaactct ccccatctcc 420
ccccctccc caccccaat tttgtattta tttatttttt aattattttg tgcagcgatg 480
ggggcggggg gggggggggc gcgcgccagg cggggcgggg cggggcgagg ggcggggcgg 540
ggcgaggcgg agaggtgcgg cggcagccaa tcagagcggc gcgctccgaa agtttccttt 600
tatggcgagg cggcgggcgg gcgggcccta taaaaagcga agcgcgcggc gggcggg 657

```

```

<210> 8
<211> 278
<212> DNA
<213> Gallus gallus

```

```

<220>
<223> avian beta-actin promoter sequence

```

```

<400> 8
tcgaggtgag cccacgttc tgcttcaactc tcccatctc cccccctcc ccacccccaa 60
ttttgtatth atttatttt taattatttt gtgcagcgat gggggcgggg gggggggggg 120
cgcgcgccag gcggggcggg gcggggcgag gggcgggcg gggcgaggcg gagaggtgcg 180
gcggcagcca atcagagcgg cgcgctccga aagtttcctt ttatggcgag gcggcgggcg 240
cggcgggcct ataaaaagcg aagcgcgcg cgggcggg 278

```

```

<210> 9
<211> 41
<212> DNA
<213> Mus musculus

```

```

<220>
<223> forward primer sequence for isolation of the IAP element used
      in Example 1

```

```

<400> 9
gcagcgggcg ccgtgggtggc acacactttt agtccccgca g 41

```

```

<210> 10
<211> 41
<212> DNA
<213> Mus musculus

```

```

<220>
<223> reverse primer sequence for isolation of the IAP element used
      in Example 1

```

```

<400> 10
ggcgactag tgatgccctc tcaggcctcc actcaggcac t 41

```

```

<210> 11
<211> 30
<212> DNA
<213> Mus musculus

```

<220>
 <223> forward primer sequence for isolation of the full length of the IAP
 element used in Example 1

<400> 11
 atgcccagat ttcttcacg gctattaggg 30

<210> 12
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> reverse primer sequence for isolation of the full length of the IAP
 element used in Example 1

<400> 12
 gatgccctct caggcctcca ctcaggcact 30

<210> 13
 <211> 40
 <212> DNA
 <213> Mus musculus

<220>
 <223> forward primer sequence related to the CMV promoter used
 in Example 1 (c)

<400> 13
 ccaagcggcc gctggccatt gcatacgttg tatccatattc 40

<210> 14
 <211> 40
 <212> DNA
 <213> Mus musculus

<220>
 <223> reverse primer sequence related to the CMV promoter used
 in Example 1 (c)

<400> 14
 gcgagaaaaa cggttcacta aacgagctct gcttatatag 40

<210> 15
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>

<223> forward primer sequence related to the R region of the IAP used
in Example 1 (c)

<400> 15
ttagtgaacc gtttttctcg ctctcttgct 30

<210> 16
<211> 30
<212> DNA
<213> Mus musculus

<220>
<223> reverse primer sequence related to the R region of the IAP used
in Example 1 (c)

<400> 16
tctgaaatga agtatccctc ctgcgccagt 30

<210> 17
<211> 63
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 17
cgaatcgtaa ccgttcgtac gagaattcgt acgagaatcg ctgtcctctc caacgagcca 60
agg 63

<210> 18
<211> 26
<212> DNA
<213> Mus musculus

<220>
<223> a linking sequence of a linker DNA used in Example 3

<400> 18
ccttggtcgt tttttttttg caaaaa 26

<210> 19
<211> 25
<212> DNA
<213> Mus musculus

<220>
<223> a linker specific primer for use in the first round
in Example 3 (forward)

<400> 19
 cgaatcgtaa ccgttcgtac gagaa 25

<210> 20
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> a linker specific primer for use in the first round
 in Example 3 (reverse)

<400> 20
 gagatgcatg ctttgcatatc ttctgcctgc 30

<210> 21
 <211> 25
 <212> DNA
 <213> Mus musculus

<220>
 <223> a linker specific primer for use in the second round
 in Example 3 (forward)

<400> 21
 tcgtacgaga atcgctgtcc tctcc 25

<210> 22
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> a linking sequence of neo cassette specific primer for use
 in the second round in Example 3 (reverse)

<400> 22
 ggagcctggg gactttccac acctggttgc 30

<210> 23
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> an alternative linking sequence of neo cassette specific primer
 for use in the second round in Example 3 (reverse)

<400> 23

ggggagcctg gggactttcc acaccctaac

30

<210> 24

<211> 39

<212> DNA

<213> Gallus gallus

<220>

<223> a primer 5' upstream until the transcription initiation site of chicken beta-actin promoter used in Example 4

<400> 24

gcaatgcggc cgcattgatt attgactagt tattaatag

39

<210> 25

<211> 39

<212> DNA

<213> Gallus gallus

<220>

<223> a primer 3' of chicken beta-actin promoter used in Example 4

<400> 25

cgagaaaaac cgcccgcgc gcgcttcgct ttttatagg

39

<210> 26

<211> 40

<212> DNA

<213> Gallus gallus

<220>

<223> an alternative primer 3' of chicken beta-actin promoter used in Example 4

<400> 26

cgagaaaaac cccgccgcc gcgcgcttcg ctttttatag

40

<210> 27

<211> 36

<212> DNA

<213> Mus musculus

<220>

<223> a primer of the 5' upstream from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 27

cgcggggggc gggtttttctc gctctcttgc ttcttg

36

<210> 28
 <211> 30
 <212> DNA
 <213> Mus musculus

<220>
 <223> a primer of the 3' side from the 5' terminus of the R region of the IAP
 to the downstream of the U5 region used in Example 4

<400> 28
 tctgaaatga agtatccctc ctgcgccagt 30

<210> 29
 <211> 36
 <212> DNA
 <213> Mus musculus

<220>
 <223> an alternative primer of the 3' side from the 5' terminus of the R region of the IAP to the downstream of the U5 region used in Example 4

<400> 29
 cggcgggcgg ggtttttctc gctctcttgc ttcttg 36

<210> 30
 <211> 903
 <212> DNA
 <213> Mus musculus

<220>
 <223> gamma globin intron sequence

<400> 30
 gtgagtcag gagatgtttc agcactgttg ctttagtct cgaggcaact tagacaactg 60
 agtattgatc tgagcacagc aggggtgtgag ctgtttgaag atactggggg tgggggtgaa 120
 gaaactgcag aggactaact gggctgagac ccagtggcaa tgttttaggg cctaaggaat 180
 gcctctgaaa atctagatgg acaactttga ctttgagaaa agagaggtgg aaatgaggaa 240
 aatgactttt ctttattaga ttctggtaga aagaactttc acctttcccc tatttttgtt 300
 attcgtttta aaacatctat ctggaggcag gacaagtatg gtcgttaaaa agatgcaggc 360
 agaaggcata tattggctca gtcaaagtgg gggaactttg gtggccaaac atacattgct 420
 aaggctattc ctatatcagc tggacacata taaaatgctg ctaatgcttc attacaaact 480
 tatatccttt aattccagat gggggcaaag tatgtccagg ggtgaggaa aattgaaaca 540
 tttgggctgg agtagatttt gaaagtcagc tctgtgtgtg tgtgtgtgtg tgtgtgtgtg 600
 tgtgtgtgtg cgcacgtgtg tttgtgtgtg tgtgagagcg tgtgtttctt ttaacgtttt 660
 cagcctacag catcacagggt tcatgggtgc aagaagataa caagatttaa attatggcca 720
 gtgactagtg ctgcaagaag aacaactacc tgcatttaat gggaaagcaa aatctcaggc 780
 tttgagggaa gttaacatag gcttgattct ggggtggaagc tgggtgtgta gttatctgga 840
 ggccaggctg gagctctcag ctcaactatg gttcatcttt attgtctcct ttcactctca 900
 cag 903

<210> 31
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a sequence of the tRNA binding site of the full length IAP

<400> 31
 tccgggacga gaaaa 15

<210> 32
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a repeat sequence of the R region of the full length IAP

<400> 32
 ttgcttcttg ctctc 15

<210> 33
 <211> 17
 <212> DNA
 <213> Mus musculus

<220>
 <223> a specific sequence for the full length IAP (tRNA binding site)

<400> 33
 tggtgccgaa ttccggg 17

<210> 34
 <211> 15
 <212> DNA
 <213> Mus musculus

<220>
 <223> a tandem repeat sequence specific for the full length IAP

<400> 34
 aatccgggac gagaa 15

<210> 35
 <211> 11
 <212> DNA
 <213> Mus musculus

<220>

<223> a repeat sequence of the R region found in the full length IAP

<400> 35

ttgcttcttg c 11

<210> 36

<211> 378

<212> DNA

<213> Mus musculus

<220>

<223> cytomegalovirus (CMV) enhancer sequence

<400> 36

attgattatt	gactagttat	taatagtaat	caattacggg	gtcattagtt	catagcccat	60
atatggagtt	ccgcgttaca	taacttacgg	taaatggccc	gcctggctga	ccgccaacg	120
acccccgccc	attgacgtca	ataatgacgt	atgttcccat	agtaacgcca	atagggactt	180
tccattgacg	tcaatgggtg	gagtatttac	ggtaaactgc	ccacttggca	gtacatcaag	240
tgtatcatat	gccaagtacg	ccccctattg	acgtcaatga	cggtaaatgg	cccgcctggc	300
attatgccca	gtacatgacc	ttatgggact	ttcctacttg	gcagtacatc	tacgtattag	360
tcacgctat	taccatgg					378

<210> 37

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the sense direction of 1st primer used
in Example 8

<400> 37

agggctgcgg caagggcaac atcctgttcg 30

<210> 38

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the antisense direction of 1st primer used
in Example 8

<400> 38

gccgccgtcc tccacgtagg tcttctccag 30

<210> 39

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the sense direction of 2nd primer used
in Example 8

<400> 39

ggcaaccagc tggcgcagat ccgcgtgacc

30

<210> 40

<211> 30

<212> DNA

<213> Artificial

<220>

<223> synthetic sequence in the antisense direction of 2nd primer used
in Example 8

<400> 40

gtccttcacc acgcccttgc tcttcacag

30

<210> 41

<211> 37

<212> DNA

<213> unknown

<220>

<223> the sequence of a junctional portion between the
CMV promoter and the R region

<400> 41

gagctcggtt agtgaaccgt tttctcgct ctcttgc

37

<210> 42

<211> 36

<212> DNA

<213> UNKNOWN

<220>

<223> the sequence of a juncture site of CA promoter

<400> 42

gaagcgcgcg gcgggcggtt tttctcgctc tcttgc

36

<210> 43

<211> 38

<212> DNA

<213> unknown

<220>

<223> the sequence of a juncture site of CA promoter

<400> 43
gaagcgcgcgcg gcgggcgggg tttttctcgc tctcttgc 38

<210> 44
<211> 60
<212> DNA
<213> UNKNOWN

<220>
<223> Sequence of the GAG gene preferable for
transposition

<400> 44
atgaattcag aacttttcac gtggggaacg agagtaccag tgagtatggt tggccttgaa 60

<210> 45
<211> 20
<212> PRT
<213> UNKNOWN

<220>
<223> Sequence of the GAG gene preferable for
transposition

<400> 45
Met Asn Ser Glu Leu Phe Ser Trp Gly Thr Arg Val Pro Val Ser Met
1 5 10 15
Phe Gly Leu Glu
20

<210> 46
<211> 15
<212> DNA
<213> unknown

<220>
<223> repeat sequence

<400> 46
tccgggacga gaaaa 15

<210> 47
<211> 15
<212> DNA
<213> Artificial Sequence

<220>
<223> repeat sequence

<400> 47
ttgcttcttg ctctc 15